

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/018, 105 A
Source: IFW16
Date Processed by STIC: 12/13/2005

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/13/2005

PATENT APPLICATION: US/10/018,105A

TIME: 16:17:30

Input Set : E:\substitute SEQLIST (10182-015-999).TXT

Output Set: N:\CRF4\12132005\J018105A.raw

4 <110> APPLICANT: MYCOTA BIOSCIENCES INC.
 5 ROEMER, Terry
 6 BUSSEY, Howard
 7 DAVISON, John
 9 <120> TITLE OF INVENTION: IDENTIFICATION OF CANDIDA ALBICANS ESSENTIAL FUNGAL
 10 SPECIFIC GENES AND USE THEREOF IN ANTIFUNGAL DRUG
 11 DISCOVERY
 13 <130> FILE REFERENCE: 10182-015-999 (originally 12875.3)
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/018,105A
 16 <141> CURRENT FILING DATE: 2002-07-15 (371c date 2000-05-05)
 18 <150> PRIOR APPLICATION NUMBER: 60/132,878
 19 <151> PRIOR FILING DATE: 1999-05-05
 21 <160> NUMBER OF SEQ ID NOS: 13
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 7558
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Candida albicans
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (2770)..(7110)
 33 <223> OTHER INFORMATION: Candida albicans KRE5
 35 <400> SEQUENCE: 1
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 38 gccaatattca agatgttgac aaagttgcgt ctatggcact accacctcta ctgggaggat 120
 40 gtgtaccctg tattgatcgt ggaggatgtc gagctccaca actgcacgtg ggagtttccg 180
 42 ttcacgctat' cgcaattcaa ttacaactcc aacatcaggc gacttgtggt gtcgtatgct 240
 44 gaaggcaacg cgtttgcggt gtctgaacgg tacagagagt ttttgcaata tggaaacgga 300
 46 gaagactttt caagtttgga ggagcttacg gtcactgtgg cgagagggag tctcaacagc 360
 48 agcgtgatgt cacggttcat gaacactggc aacttcccga gactaagagc attgcggggt 420
 50 cttgcaaggg aaggcgcata caacctatcg cattggtttg gaaagttgcc gacaaaacag 480
 52 tacgttgcggt gtactagaca tgcaggtgga ttacgaagct cgtgaccggg agagagcatt 540
 54 gaaggaggcc aatagatact ttccattcct tgatgtgaag atacatagac cataaaagca 600
 56 caaggctgcg aatatatatac gcgtatagac tctactaata aacatccaaa ccagagtga 660
 58 aaaaaaaaaat acaacacaaa ccagaaaaaa aacaaacgaa ccacttaca gacccatctc 720
 60 taccacaaca ccaatgtact ggggtgctact ccttttcgtg tcgatatgca tggccaacac 780
 62 ggagacatgc ttggtacggg tgcccagagta ctacaatatt gtaccgcacc cgtcacccat 840
 64 atccagggat gccagggttca gtcgcgagct ccacgtctc aacaccaccc acacagtact 900
 66 actagactac cccattggat ctatcgacga ccaggatatg tccaacataa tcacagtcac 960
 68 atacgatacc gttgcgcaac cagcatcaac actactagtg cgcgtaaca actacggaga 1020
 70 caatacgttt acgaacggcg acatgctcaa cattaagcta tgctggccgg ccaccatgcc 1080
 72 gtacgacttt agcattgacc atgtgtatat gcacagcaac gagttggttg agagtgtgga 1140
 74 ggatgagttt gatttgatat tggcggtcac ctacgagttc catgccttta gttatgacaa 1200

cp9-6)

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76 tgggagggttt ttgcaagaag aaacggcatt gtccttccaa ttgtacgtga acaaattgcc 1260
78 cagtagattc ttaccattc cattggagtt gtacgaaaca atcgtgtatt tagtagatat 1320
80 cacaatattc attgtctgga acatcttgcc atatttggtt aagggtgtat tagaagccgt 1380
82 ggggcagtag tggtgcgtta tattttaagg aaaataaaca aatgatttta tcaagtcgat 1440
84 tagccttata acattagctg atatgtttgt tggctctatag gttttaatga tattgttaga 1500
86 ttaaggttt gctttgtagc tggcaaagt tagatgccaa ttcgttgggg tcgtgttcac 1560
88 taccaatact gcagtaaaaa cgagtttgac tctttgtata atatttagct cattcgcaga 1620
90 tcaaataatt cgttcttttc taggtgccac actagcaaaa ggttatgggt aaagaaggac 1680
92 acggtgcatt tcctgttcct aaagccaatg acataccgcc tcctgcaaat ataaagaaga 1740
94 tcggggcctt gaaacgtttt tcagatgaag cttatgcgaa gtctttgctc tatgatgcag 1800
96 caagattagt tgcaccaata atacacgagc agaagttcaa agttggaaaa ttatatgaaa 1860
98 tgtatcctga taaggcggaa ctatggggcc taaatgtcaa tcacggacaa aagatatacc 1920
100 taaggttaag agaacatcac aatgataaac tgtttctccc catgggtgat atagtaggga 1980
102 ccttacttca tgaattaaca cacaaattgt atagtgtca cgatagtaag ttctacaagt 2040
104 ttttgacaa actaaagtcg agatacgacg acatacattg taggggagcc aaaacaaaat 2100
106 atttatgcga ggaaaacaag gttggtagag gtgtattatt atccggaagt ttagtatctg 2160
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112 caattctaga ggcggcagag cgtcggttga gagattcaaa atgggtgcat agtgaatg 2340
114 cagaaaccga aagtgttccc aaagaggacg agtacgacac aactcaggtg gagcttatcg 2400
116 gtcctacaga aggtaaacca gttggaacat ttgctaata tatcattgat ttaacatcg 2460
118 aactgaaga aactccaatt caacctgata acccgaaacg ccgcatactc cagcagataa 2520
120 ttgatttaac tcagataca gaagacatag agccaacatc accagaggta atatgtatag 2580
122 attaagttaa atataaaggc aaatatattg ccaatgtaat actcttttaa cagtgttggt 2640
124 ctctgcaag gattaagcac cgaaaaaaa tatgtggatg cgttgttatt agttttactc 2700
126 tttgctttt ctgaaaagaa acattaacgt gttctactag tttgtcacac tacgacacaa 2760
128 gtccttgaa atg tca ttt gca agg tat atc tac tac acc att gcg gtt gct 2811
129 Met Ser Phe Ala Arg Tyr Ile Tyr Tyr Thr Ile Ala Val Ala
130 1 5 10
132 gtt tta tta aat ttt gtc aaa gct act gaa aat aac aat ttt aaa ctt 2859
133 Val Leu Leu Asn Phe Val Lys Ala Thr Glu Asn Asn Asn Phe Lys Leu
134 15 20 25 30
136 gaa gtt gaa gcg tca tgg agc aat att gat ttc ctt cct agc ttt ata 2907
137 Glu Val Glu Ala Ser Trp Ser Asn Ile Asp Phe Leu Pro Ser Phe Ile
138 35 40 45
140 gag gcc atc gtt ggc ttc aat gac tct ttg tac gaa cag aca att gaa 2955
141 Glu Ala Ile Val Gly Phe Asn Asp Ser Leu Tyr Glu Gln Thr Ile Glu
142 50 55 60
144 aca att ttt ggt tta gga gac act gaa gtg gaa tta gaa gat gat gct 3003
145 Thr Ile Phe Gly Leu Gly Asp Thr Glu Val Glu Leu Glu Asp Asp Ala
146 65 70 75
148 tca gat caa gaa ata tat tct acc gtg atc aac tca tta ggg tta aca 3051
149 Ser Asp Gln Glu Ile Tyr Ser Thr Val Ile Asn Ser Leu Gly Leu Thr
150 80 85 90
152 gat caa gat ttg gat ttt att aat ttt gat tta acc aac aaa aaa cat 3099
153 Asp Gln Asp Leu Asp Phe Ile Asn Phe Asp Leu Thr Asn Lys Lys His
154 95 100 105 110
156 aca cca aga atc gca gcc cat tac gat cac tat tct gat gtt cta act 3147
157 Thr Pro Arg Ile Ala Ala His Tyr Asp His Tyr Ser Asp Val Leu Thr

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160 aag ttt ggc gat cga ctc aaa agt gaa tgt gca aaa gac tct ttt ggg 3195
161 Lys Phe Gly Asp Arg Leu Lys Ser Glu Cys Ala Lys Asp Ser Phe Gly
162          130          135          140
164 aat gca gtg gaa acg aaa aat ggt caa att caa acg tgg tta cta tat 3243
165 Asn Ala Val Glu Thr Lys Asn Gly Gln Ile Gln Thr Trp Leu Leu Tyr
166          145          150          155
168 aac gat aag ata tat tgt tgc gct aat gat ttg ttt gca tta cga act 3291
169 Asn Asp Lys Ile Tyr Cys Ser Ala Asn Asp Leu Phe Ala Leu Arg Thr
170          160          165          170
172 gat ttg agt tct cat tct aca ctt tta ttt gat agg att att gga aaa 3339
173 Asp Leu Ser Ser His Ser Thr Leu Leu Phe Asp Arg Ile Ile Gly Lys
174 175          180          185          190
176 tca aaa gat gca cct ttg gtg att tta tat gga agc ccg act gag gaa 3387
177 Ser Lys Asp Ala Pro Leu Val Ile Leu Tyr Gly Ser Pro Thr Glu Glu
178          195          200          205
180 ctg act aaa gat ttt ctt aaa ata ttg tat cca gat gca aag gct gga 3435
181 Leu Thr Lys Asp Phe Leu Lys Ile Leu Tyr Pro Asp Ala Lys Ala Gly
182          210          215          220
184 aaa tta aag ttt gta tgg agg tac att cca ctg gga atc aaa aaa ctg 3483
185 Lys Leu Lys Phe Val Trp Arg Tyr Ile Pro Leu Gly Ile Lys Lys Leu
186          225          230          235
188 gac tca att tct gga tac ggt gta tca ttg aaa atg gaa aag tat gat 3531
189 Asp Ser Ile Ser Gly Tyr Gly Val Ser Leu Lys Met Glu Lys Tyr Asp
190          240          245          250
192 tat tct ggt gca gaa gga aat cca aag tat gat ttg agt cga gat ttc 3579
193 Tyr Ser Gly Ala Glu Gly Asn Pro Lys Tyr Asp Leu Ser Arg Asp Phe
194 255          260          265          270
196 acc aga att aat gac tgc caa gag ttg gtc ctg gtc aat gaa aaa cat 3627
197 Thr Arg Ile Asn Asp Ser Gln Glu Leu Val Leu Val Asn Glu Lys His
198          275          280          285
200 tgc tat gaa ctt ggt gtt aaa ttg act tca ttc ata tta tcc aat cgt 3675
201 Ser Tyr Glu Leu Gly Val Lys Leu Thr Ser Phe Ile Leu Ser Asn Arg
202          290          295          300
204 tac aag agt act aaa tat gac ctt tta gat acg att tta acc aac ttt 3723
205 Tyr Lys Ser Thr Lys Tyr Asp Leu Leu Asp Thr Ile Leu Thr Asn Phe
206          305          310          315
208 ccc aag ttt att cct tac att gca cga tta cca aaa tta cta aat cat 3771
209 Pro Lys Phe Ile Pro Tyr Ile Ala Arg Leu Pro Lys Leu Leu Asn His
210          320          325          330
212 gaa aaa gtt aaa tcc aaa gtg ctt gga aat gaa gat ata ggg cta tct 3819
213 Glu Lys Val Lys Ser Lys Val Leu Gly Asn Glu Asp Ile Gly Leu Ser
214 335          340          345          350
216 caa gac tcc tac gga ata tat atc aac ggt tcc cca ata aat cca cta 3867
217 Gln Asp Ser Tyr Gly Ile Tyr Ile Asn Gly Ser Pro Ile Asn Pro Leu
218          355          360          365
220 gag tta gat att tac aat cta ggt acc agg ata aag gag gaa tta cag 3915
221 Glu Leu Asp Ile Tyr Asn Leu Gly Thr Arg Ile Lys Glu Glu Leu Gln
222          370          375          380

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224 act gtg aaa gat tta gtg aaa ctt gga ttt gat acc gta caa gca aag 3963
225 Thr Val Lys Asp Leu Val Lys Leu Gly Phe Asp Thr Val Gln Ala Lys
226      385      390      395
228 ctc ttg ata gca aaa ttt gct tta ctt tca gct gtt aaa caa aca caa 4011
229 Leu Leu Ile Ala Lys Phe Ala Leu Leu Ser Ala Val Lys Gln Thr Gln
230      400      405      410
232 ttt cga aat ggg aat aca tta atg ggt aac aat gaa aat aga ttt aaa 4059
233 Phe Arg Asn Gly Asn Thr Leu Met Gly Asn Asn Glu Asn Arg Phe Lys
234 415      420      425      430
236 gtg tat gaa aat gaa ttt aag aag ggt agt tca gaa aag ggt ggg gtc 4107
237 Val Tyr Glu Asn Glu Phe Lys Lys Gly Ser Ser Glu Lys Gly Gly Val
238      435      440      445
240 ttg ttt ttc aat aac att gaa tta gac aac aca ttc aag gag tac acc 4155
241 Leu Phe Phe Asn Asn Ile Glu Leu Asp Asn Thr Phe Lys Glu Tyr Thr
242      450      455      460
244 act gat cgt gag gag gca tat tta gga gtt ggt tct cat aaa ctt aag 4203
245 Thr Asp Arg Glu Glu Ala Tyr Leu Gly Val Gly Ser His Lys Leu Lys
246      465      470      475
248 cca aat caa att ccg tta ttg aaa gag aac atc cat gat tta att ttc 4251
249 Pro Asn Gln Ile Pro Leu Leu Lys Glu Asn Ile His Asp Leu Ile Phe
250      480      485      490
252 gca tta aat ttt ggg aac aaa aac caa ttg cgg gtg ttt ttc act tta 4299
253 Ala Leu Asn Phe Gly Asn Lys Asn Gln Leu Arg Val Phe Phe Thr Leu
254 495      500      505      510
256 tct aag gtg att ttg gac tcc ggt ata cct caa caa gtt gga gtt ttg 4347
257 Ser Lys Val Ile Leu Asp Ser Gly Ile Pro Gln Gln Val Gly Val Leu
258      515      520      525
260 ccc gtt ata gga gat gac cca atg gat ctg tta ctc gct gag aaa ttt 4395
261 Pro Val Ile Gly Asp Asp Pro Met Asp Leu Leu Leu Ala Glu Lys Phe
262      530      535      540
264 tat tgg att gct gag aaa tca agc aca caa gag gca tta gca ata ttg 4443
265 Tyr Trp Ile Ala Glu Lys Ser Ser Thr Gln Glu Ala Leu Ala Ile Leu
266      545      550      555
268 tat aaa tat ttt gaa tca aac agt cca gat gaa gtt gat gac tta tta 4491
269 Tyr Lys Tyr Phe Glu Ser Asn Ser Pro Asp Glu Val Asp Asp Leu Leu
270      560      565      570
272 gat aaa gtg gaa gta ccc gaa gat tat aaa gtg gat tat aat cat gtg 4539
273 Asp Lys Val Glu Val Pro Glu Asp Tyr Lys Val Asp Tyr Asn His Val
274 575      580      585      590
276 tta aac aag ttt tct ata tca act gct tcg gtc att ttc aat ggg gtt 4587
277 Leu Asn Lys Phe Ser Ile Ser Thr Ala Ser Val Ile Phe Asn Gly Val
278      595      600      605
280 att tac gat tta aga gca cca aac tgg cag att gca atg agt aaa caa 4635
281 Ile Tyr Asp Leu Arg Ala Pro Asn Trp Gln Ile Ala Met Ser Lys Gln
282      610      615      620
284 ata tcc cag gac att tca ctt att aaa act ttc ttg aga cag gga cca 4683
285 Ile Ser Gln Asp Ile Ser Leu Ile Lys Thr Phe Leu Arg Gln Gly Pro
286      625      630      635
288 ata gag ggt aga ttg aaa gat gtt ctt tac tct aat gca aaa tca gaa 4731

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289 Ile Glu Gly Arg Leu Lys Asp Val Leu Tyr Ser Asn Ala Lys Ser Glu
290      640                      645                      650
292 cgc aat tta cgt ata att cca tta gaa cct agt gac att att tac aag 4779
293 Arg Asn Leu Arg Ile Ile Pro Leu Glu Pro Ser Asp Ile Ile Tyr Lys
294 655                      660                      665                      670
296 aaa atc gac aag gaa tta ata aac aat tca att gca ttc aag aag cta 4827
297 Lys Ile Asp Lys Glu Leu Ile Asn Asn Ser Ile Ala Phe Lys Lys Leu
298                      675                      680                      685
300 gat aaa gcg cag ggt gtg tct gga aca ttt tgg cta gtg tcg gat ttt 4875
301 Asp Lys Ala Gln Gly Val Ser Gly Thr Phe Trp Leu Val Ser Asp Phe
302                      690                      695                      700
304 acc aag tca gca ata att act caa ttg ata gat ttg tta ttg ctt ctc 4923
305 Thr Lys Ser Ala Ile Ile Thr Gln Leu Ile Asp Leu Leu Leu Leu
306                      705                      710                      715
308 aaa aag aaa gca att cag ata aga att att aat act ggg gat aca gat 4971
309 Lys Lys Lys Ala Ile Gln Ile Arg Ile Ile Asn Thr Gly Asp Thr Asp
310                      720                      725                      730
312 gtt ttt gga aaa ttg aaa aca aag ttt aaa tta acc gcc tta aca aat 5019
313 Val Phe Gly Lys Leu Lys Thr Lys Phe Lys Leu Thr Ala Leu Thr Asn
314 735                      740                      745                      750
316 gga caa att gat gaa att att gag att ttg aaa aaa tcc aac gct tca 5067
317 Gly Gln Ile Asp Glu Ile Ile Glu Ile Leu Lys Lys Ser Asn Ala Ser
318                      755                      760                      765
320 agt gca aat aat gat gaa ttg aaa aaa atg ctt gag act aag caa tta 5115
321 Ser Ala Asn Asn Asp Glu Leu Lys Lys Met Leu Glu Thr Lys Gln Leu
322                      770                      775                      780
324 cct gct cat cac tct ttt ttg cta ttc aac tct aga tat ttt aga ttg 5163
325 Pro Ala His His Ser Phe Leu Leu Phe Asn Ser Arg Tyr Phe Arg Leu
326                      785                      790                      795
328 gat gga aat ttt gga tac gag gaa ttg gat caa att ata gag ttt gaa 5211
329 Asp Gly Asn Phe Gly Tyr Glu Leu Asp Gln Ile Ile Glu Phe Glu
330                      800                      805                      810
332 gta tct caa aga ttg aac tta atc ccg gac atc atg gag gca tat ccg 5259
333 Val Ser Gln Arg Leu Asn Leu Ile Pro Asp Ile Met Glu Ala Tyr Pro
334 815                      820                      825                      830
336 gat gag ttt agg tcg aag aag gta agt gat ttt aat ctg gtt ttg tct 5307
337 Asp Glu Phe Arg Ser Lys Lys Val Ser Asp Phe Asn Leu Val Leu Ser
338                      835                      840                      845
340 gga tta gac aat atg gac tgg ttt gat ttg gtg act tcc ata gtg aca 5355
341 Gly Leu Asp Asn Met Asp Trp Phe Asp Leu Val Thr Ser Ile Val Thr
342                      850                      855                      860
344 aaa tca ttc cat gtc gac gaa aaa agg ttt att gtt gat gtt aac agg 5403
345 Lys Ser Phe His Val Asp Glu Lys Arg Phe Ile Val Asp Val Asn Arg
346                      865                      870                      875
348 ttt gat ttt agc tca ttg gat ttt tca aac tcg att gat gta acg act 5451
349 Phe Asp Phe Ser Ser Leu Asp Phe Ser Asn Ser Ile Asp Val Thr Thr
350                      880                      885                      890
352 tat gaa gaa aat agt cca gtt gat gta tta ata att ttg aac cct atg 5499
353 Tyr Glu Glu Asn Ser Pro Val Asp Val Leu Ile Ile Leu Asn Pro Met

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/13/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 182,3408

Seq#:5; N Pos. 16,33,131,554,5240,5266,5293

VERIFICATION SUMMARY

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Input Set : E:\substitute SEQLIST (10182-015-999).TXT

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:16 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:180
L:1060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:3383
L:1265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:1269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:120
L:1283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:540
L:1568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:5238